

(1) GENERAL INFORMATION:

(i) APPLICANT: Simons, Michael
Volk, Rudiger
Horowitz, Arie

(ii) TITLE OF INVENTION: Stimulation of angiogenesis
via enhanced endothelial expression of syndecan-4
core proteins

(iii) NUMBER OF SEQUENCES: 24

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David Prashker, Esq.
(B) STREET: P.O. Box 5387
(C) CITY: Magnolia
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 01930

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
(B) COMPUTER: Dell PC
(C) OPERATING SYSTEM: MS DOS
(D) SOFTWARE: Microsoft Word version 97

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/145,916
(B) FILING DATE: September 2, 1998
(C) CLASSIFICATION: Unknown

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: David Prashker, Esq.
(B) REGISTRATION NUMBER: 29,693
(C) REFERENCE/DOCKET NUMBER: BIS-039

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (978) 525-3794

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ATGAGACGTG CGGCGCTCTG GCTTTGGCTC TGCGCGCTGG CGCTGCGCCT GCAGCCTGCC 60
CTCCCGCAAA TTGTCACCGC AAATGTGCCT CCTGAAGACC AAGATGGCTC TGGGGACGAC 120
TCAGACAACT TCTCTGGCTC AGGCACAGGT GCTTTGCCAG ATATGACTTT GTCACGGCAG 180
ACACCTTCCA CTTGGAAGGA TGTGTGGCTC CTGACAGCTA CACCCACAGC TCCAGAACCC 240
ACCAGCAGGG ATACCGAGGC CACCTCACC TCTATCCTGC CGGCTGGAGA GAAGCCTGAG 300
GAGGGAGAGC CCGTGGCCCA CGTGAAGCA GAGCCTGACT TCACTGCTCG GGACAAGGAG 360
AAGGAGGCCA CCACCAGGCC TAGGGAGACC ACACAGCTCC CAGTCACCCA ACAGGCCTCA 420
ACAGCAGCCA GAGCCACCAC GGCCCAGGCA TCTGTACGT CTCATCCCCA CGGGGATGTG 480
CAACCTGGCC TCCACGAGAC CTTGGCTCCC ACAGCACCCG GCCAACCTGA CCATCAGCCT 540
CCAAGTGTGG AGGATGGAGG CACTTCTGTC ATCAAAGAGG TTGTGGAGGA TGAAACTACC 600
AATCAGCTTC CTGCAGGAGA GGGCTCTGGA GAACAAGACT TCACCTTTGA AACATCTGGG 660
GAGAACACAG CTGTGGCTGG CGTCGAGCCT GACCTTCGGA ATCAGTCCCC AGTGGATGAA 720
GGAGCCACAG GTGCTTCTCA GGGCCTTTTG GACAGGAAGG AA 762

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1020 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

GGCAGGAGGG AGGGAGCCAG AGGAAAAGAA GAGGAGGAGA AGGAGGAGGA CCGGGGAGG 60
GAGGCGCGGC GCGGGAGGAG GAGGGGCGCA GCCGCGGAGC CAGTGGCCCC GCTTGACGC 120
GCTGCTCTCC AGATACCCCC GGAGCTCCAG CCGCGCGGAT CGCGCGCTCC CGCGCTCTG 180
CCCCTAAACT TCTGCCGTAG CTCCCTTTCA AGCCAGCGAA TTTATTCCTT AAAACCAGAA 240
ACTGAACCTC GGCACGGGAA AGGAGTCCGC GGAGGAGCAA AACCACAGCA GAGCAAGAAG 300
AGCTTCAGAG AGCAGCCTTC CCGGAGCACC AACTCCGTGT CGGGAGTGCA GAAACCAACA 360
AGTGAGAGGG CGCCCGGTTT CCGGGGCGCA GCTGCGGGCG GCGGGAGCAG GCGCAGGAGG 420
AGGAAGCGAG CGCCCGGAG CCGCGAGCCG GAGTCCCGA GCCTGAGCCG CAATCGCTGC 480
GGTACTCTGC TCCGGATTCT TGTGCGCGGG CTGCGCGAGC GCTGGGCAGG AGGCTTCGTT 540
TTGCCCTGGT TGCAAGCAGC GGCTGGGAGC AGCCGGTCCC TGGGAATAT CGGCGCGCGG 600
TGGATCTGCT TCACCTTGGG CTTGGTGGCC TGGGTGTCGG CGGAGTCGAG AGCAGAGCTG 660
ACATCTGATA AAGACATGTA CCTTGACAAC AGCTCCATTG AAGAAGCTTC AGGAGTGTAT 720
CCTATTGATG ACGATGACTA CGCTTCTGCG TCTGGCTCGG GAGCTGATGA GGATGTAGAG 780
AGTCCAGAGC TGACAACAAC TCGACCACTT CCAAAGATAC TGTGACTAG TGCTGCTCCA 840
AAAGTGGAAA CCACGACGCT GAATATACAG AACAAAGATAC CTGCTCAGAC AAAGTCACCT 900
GAAGAACTG ATAAGAGAA AGTTCACCTC TCTGACTCAG AAAGGAAAAT GGACCCAGCC 960
GAAGAGGATA CAAATGTGTA TACTGAGAAA CACTCAGACA GTCTGTTTAA ACGGACAGAA 1020

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(2) INFORMATION FOR SEQ ID NO:3:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Gly Arg Arg Glu Gly Ala Arg Gly Lys Glu Glu Glu Lys Glu Glu
1           5           10           15
Asp Pro Gly Arg Glu Ala Arg Arg Gly Arg Arg Arg Gly Ala Ala Ala
20           25           30
Glu Pro Val Ala Pro Leu Gly Arg Ala Ala Leu Gln Ile Pro Pro Glu
35           40           45
Leu Gln Pro Arg Gly Ser Arg Ala Pro Ala Ala Leu Pro Leu Asn Phe
50           55           60
Cys Arg Ser Ser Leu Ser Ser Gln Arg Ile Tyr Ser Leu Lys Pro Glu
65           70           75           80
Thr Glu Pro Arg His Gly Lys Gly Val Arg Gly Gly Ala Lys Pro Gln
85           90           95
Gln Ser Lys Lys Ser Phe Arg Glu Gln Pro Ser Arg Ser Thr Asn Ser
100          105          110
Val Ser Gly Val Gln Lys Pro Thr Ser Glu Arg Ala Pro Arg Ser Arg
115          120          125
Gly Ala Ala Ala Gly Gly Gly Ser Arg Arg Arg Arg Arg Lys Arg Ala
130          135          140
Pro Pro Ser Pro Glu Pro Glu Ser Pro Ser Leu Ser Arg Asn Arg Cys
145          150          155          160
Gly Thr Leu Leu Arg Ile Arg Val Arg Gly Leu Ala Glu Arg Trp Ala
165          170          175
Gly Gly Phe Val Leu Pro Trp Leu Gln Ala Ala Ala Gly Ser Ser Arg
180          185          190
Ser Leu Gly Asn Met Arg Arg Ala Trp Ile Leu Leu Thr Leu Gly Leu
195          200          205
Val Ala Cys Val Ser Ala Glu Ser Arg Ala Glu Leu Thr Ser Asp Lys
210          215          220

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Asp Met Tyr Leu Asp Asn Ser Ser Ile Glu Glu Ala Ser Gly Val Tyr
 225 230 235 240
 Pro Il Asp Asp Asp Tyr Ala Ser Ala Ser Gly Ser Gly Ala Asp
 245 250 255
 Glu Asp Val Glu Ser Pro Glu Leu Thr Thr Thr Arg Pro Leu Pro Lys
 260 265 270
 Ile Leu Leu Thr Ser Ala Ala Pro Lys Val Glu Thr Thr Thr Leu Asn
 275 280 285
 Ile Gln Asn Lys Ile Pro Ala Gln Thr Lys Ser Pro Glu Glu Thr Asp
 290 295 300
 Lys Glu Lys Val His Leu Ser Asp Ser Glu Arg Lys Met Asp Pro Ala
 305 310 315 320
 Glu Glu Asp Thr Asn Val Tyr Thr Glu Lys His Ser Asp Ser Leu Phe
 325 330 335
 Lys Arg Thr Glu
 340

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1079 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGCGGCGCG GCTGCTGAGC CGTCCTTGCG GCACGSSGAT GCGCGCGGAG CTGCGGCGGCC 60
 TCGCGGTGCT GCTGCTGCTG CTCAGCGCCC GCGCAGCGCT GGCTCAGCCG TGGCGCAATG 120
 AGAACTACGA GAGGCGGGTG GACCTGGAGG GCTCTGGGGA TGATGATCCC TTTGGGGACG 180
 ATGAACTGGA TGACATCTAC TCGGGCTCCG GCTCAGGCTA TTTTGAGCAG GAGTCAGGGT 240
 TGGAGACAGC GGTGACCTC ACCACGGACA CGTCCGTCCC ACTGCCCACC ACGGTGGCCG 300
 TGCTGCCTGT CACCTTGGTG CAGCCCATGG CAACACCCTT TGAGCTGTTC CCCACAGAGG 360
 ACACGTCCCC TGAGCAAACA ACCAGCGTCT TGTATATCCC CAAGATAACA GAAGCACCAG 420
 TGATCCCCAG CTGGAACAACA ACCACCGCCA GTACCACTGC CAGTGACTCC CCCAGTACCA 480
 CCTCCACCAC CACCACCACG GCTGCTACCA CCACCACAAC CACCACCACC ATCAGCACCA 540
 CTGTGGCCAC CTCCAAGCCC ACCACTACCC AGAGGTTCTT GCGGCGCTTT GTCACCAAGG 600
 CAGCCACCAC CCGGGCCACC ACCCTGGAGA CGCCACCAC CTCCATCCCT GAAACCAAGT 660
 TCCTGACAGA GGTGACCACA TCACGGCTTG TCCCTCCAG CACAGCCAAG CCGAGGTCCC 720
 TGCCAAAACC AAGCACTTCC AGGACTGCAG AACCACGGA AAAAAGCACT GCCTTGCTT 780
 CCAGCCCCAC CACGCTGCCA CCCACAGAAG CCCCCAGGT GGAGCCAGGG GAGTTGACGA 840
 CAGTCCTCGA CAGTGACCTG GAAGTCCCAA CCAGTAGTGG CCCCAGCGGG GACTTCGAGA 900
 TCCAGGAGGA GGAGGAGACA ACTCGTCCTG AGCTGGGCAA TGAGGTGGTG GCAGTGGTGA 960
 CACCACCAGC AGCACCGGGG CTGGGCAAGA ATGCAGAGCC GGGGCTCATC GACAACACAA 1020
 TAGAGTCGGG CAGCTCGGCT GCTCAGCTCC CCCAGAAAAA CATCCTGGAG AGGAAGGAA 1079

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCGCCTG TCTGCCTGTT TGCGCCGCTG CTGCTGTTGC TCCTCGGAGG TTTCCCCGTC 60
 GCGCCAGGCG AGTCGATTCT AGAGACTGAG GTCATAGACC CCCAGGACCT OCTGGAAGGC 120
 AGATACTTCT CTGGAGCCCT CCCGGACGAT GAAGACGCTG GGGGCCCTGA GCAGGACTCT 180
 GACTTTGAGC TGTCGGGTTT CCGAGATCTA GATGACACGG AGGAGCCAG GACCTTCCCT 240
 GAGGTGATTT CACCCTTGGT GCCACTAGAT AACCACATCC CCGAGAATGC CCAGCCTGSC 300

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ATCCGTGTCC CCTCAGAGCC CAAGGAACTG GAAGAGAATG AGGTCATTCC CAAAAGGGTC 360
 CCCTCCGACG TGGGGGATGA CGATGTGTCC AACAAAGTGT CCATGTCCAG CACTTCCCAG 420
 GGCAGCAACA TTTTGAAG AACTGAG 447

(2) INFORMATION FOR SEQ ID NO:6:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1590 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGGAGCTCC GGGCCCGAGG CTGGTGGCTG CTGTGCGCGG CCGCCGCGCT AGTCGCCTGC 60
 GCCC GCGGG ACCCCGCCAG CAAGAGCCGG AGCTGCAGCG AAGTCCGCCA GATCTACGGG 120
 GCTAAGGGCT TTAGCCTGAG CGACGTGCCC CAGGCAGAGA TCTCGGGAGA GCACCTGCGG 180
 ATCTGCCCC AGGGCTACAC CTGCTGCACC AGTGAGATGG AGGAGAACCT GGCCAACCAC 240
 AGCCGGATGG AGCTGGAGAC CGCACTCCAC GACAGCAGCC GTGCCCTGCA GGCTACACTG 300
 GCCACCCAGC TGCATGGCAT CGATGACCAC TTCCAGCGCC TGCTGAATGA CTCGGAGCGT 360
 ACACTGCAGG ATGCTTTTCC CGGGGCCTTT GGGGACCTGT ACACGCAGAA CACTCGGGCC 420
 TTCCGGGACC TGTATGCTGA GCTGCGTCTC TACTACCGAG GGGCCAACCT ACACCTTGAG 480
 GAGACACTGG CCGAGTCTG GGCACGGCTG CTGGAGCGTC TCTTCAAGCA GCTGCACCCC 540
 CAGCTTCTGC TGCCCGATGA CTATCTGGAC TGCCTGGGCA AGCAGGCAGA GGCCTGCGG 600
 CCGTTTGGGG ATGCCCCTCG AGAACTGCGC CTGAGGGCCA CCCGTGCTTT TGTGGCGGCA 660
 CGATCCTTTG TGCAGGGCCT GGGTGTGGCC AGTGACGTAG TCCGAAAGGT GGCCAGGTT 720
 CCTCTGGCCC CAGAATGTT TCGGGCTGTC ATGAAGTTGG TCTACTGTGC CCATTGCCGG 780
 GGAGTCCCTG GTGCCCGGCC CTGTCCCGAC TATTGCCGAA ATGTGCTCAA AGGCTGCCTT 840
 GCCAACCAGG CCGACCTGGA TGCCGAGTGG AGGAACCTCC TGGACTCCAT GGTGCTCATC 900
 ACTGACAAGT TCTGGGGCCC GTCGGGTGCG GAGAATGTCA TTGGCAGTGT GCATATGTGG 960
 CTGGCGGAGG CCATCAACGC CCTCCAGGAC AACAAGGACA CACTCACAGC TAAGGTCATC 1020
 CAGGGCTGCG GAAACCCCAA GGTCAATCCC CATGGCTCTG GGCCTGAGGA GAAGCGTCGC 1080
 CGTGGCAAAC TGGCACTGCA GGAGAAGTCC TCCACAGGTA CTCTGGAAAA GCTGGTCTCT 1140
 GAGGCCAAGG CCCAGCTCCG AGACATTCAG GACTACTGGA TCAGCCTCCC AGGGACACTG 1200
 TGTAGTGAGA AGATGGCCAT GAGTCCTGCC AGCGATGACC GCTGCTGGAA TGGGATTTCC 1260
 AAGGGCCGGT ACCTACCTGA GGTGATGGGT GATGGGCTGG CCAACCAGAT CAACAACCT 1320
 GAAGTGGAGG TGGACATCAC CAAGCCGGAT ATGACCATCC GGCAGCAGAT CATGCAGCTC 1380
 AAGATCATGA CCAACCGTTT ACGTGGCGCC TACGGTGGCA ATGATGTGGA CTCCAGGAT 1440
 GCCAGTGATG ACGGCAGTGG CTCCGGCAGC GGTGGCGGAT GCCCAGATGA CGCCTGTGGC 1500
 CGGAGGGTCA GCAAGAAGAG CTCCAGCTCC CGGACCCCTT TGACCCATGC CCTCCCCGGC 1560
 TTGTCAGAAC AGGAGGGACA GAAGACCTCG 1590

(2) INFORMATION FOR SEQ ID NO:7:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala
 1 5 10 15
 Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
 20 25 30
 Ser Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
 35 40 45
 Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
 50 55 60
 Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn His

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65					70					75				80
Ser	Arg	Met	Glu	Leu	Glu	Thr	Ala	Leu	His	Asp	Ser	Ser	Arg	Ala
				85					90					95
Gln	Ala	Thr	Leu	Ala	Thr	Gln	Leu	His	Gly	Ile	Asp	Asp	His	Phe
			100					105					110	Gln
Arg	Leu	Leu	Asn	Asp	Ser	Glu	Arg	Thr	Leu	Gln	Asp	Ala	Phe	Pro
			115					120				125		Gly
Ala	Phe	Gly	Asp	Leu	Tyr	Thr	Gln	Asn	Thr	Arg	Ala	Phe	Arg	Asp
			130					135			140			Leu
Tyr	Ala	Glu	Leu	Arg	Leu	Tyr	Tyr	Arg	Gly	Ala	Asn	Leu	His	Leu
145					150					155				160
Glu	Thr	Leu	Ala	Glu	Phe	Trp	Ala	Arg	Leu	Leu	Glu	Arg	Leu	Phe
				165					170					175
Gln	Leu	His	Pro	Gln	Leu	Leu	Leu	Pro	Asp	Asp	Tyr	Leu	Asp	Cys
			180					185					190	Leu
Gly	Lys	Gln	Ala	Glu	Ala	Leu	Arg	Pro	Phe	Gly	Asp	Ala	Pro	Arg
			195					200				205		Glu
Leu	Arg	Leu	Arg	Ala	Thr	Arg	Ala	Phe	Val	Ala	Ala	Arg	Ser	Phe
			210				215				220			Val
Gln	Gly	Leu	Gly	Val	Ala	Ser	Asp	Val	Val	Arg	Lys	Val	Ala	Gln
225					230					235				240
Pro	Leu	Ala	Pro	Glu	Cys	Ser	Arg	Ala	Val	Met	Lys	Leu	Val	Tyr
				245					250					255
Ala	His	Cys	Arg	Gly	Val	Pro	Gly	Ala	Arg	Pro	Cys	Pro	Asp	Tyr
			260					265					270	Cys
Arg	Asn	Val	Leu	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp
			275				280					285		Ala
Glu	Trp	Arg	Asn	Leu	Leu	Asp	Ser	Met	Val	Leu	Ile	Thr	Asp	Lys
			290				295				300			Phe
Trp	Gly	Pro	Ser	Gly	Ala	Glu	Asn	Val	Ile	Gly	Ser	Val	His	Met
305					310					315				320
Leu	Ala	Glu	Ala	Ile	Asn	Ala	Leu	Gln	Asp	Asn	Lys	Asp	Thr	Leu
				325					330					335
Ala	Lys	Val	Ile	Gln	Gly	Cys	Gly	Asn	Pro	Lys	Val	Asn	Pro	His
			340					345				350		Gly
Ser	Gly	Pro	Glu	Glu	Lys	Arg	Arg	Gly	Lys	Leu	Ala	Leu	Gln	Glu
			355				360				365			
Lys	Ser	Ser	Thr	Gly	Thr	Leu	Glu	Lys	Leu	Val	Ser	Glu	Ala	Lys
			370			375					380			Ala
Gln	Leu	Arg	Asp	Ile	Gln	Asp	Tyr	Trp	Ile	Ser	Leu	Pro	Gly	Thr
385					390					395				400
Cys	Ser	Glu	Lys	Met	Ala	Met	Ser	Pro	Ala	Ser	Asp	Asp	Arg	Cys
				405					410					415
Asn	Gly	Ile	Ser	Lys	Gly	Arg	Tyr	Leu	Pro	Glu	Val	Met	Gly	Asp
				420				425				430		Gly
Leu	Ala	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Glu	Val	Asp	Ile	Thr
			435				440					445		Lys
Pro	Asp	Met	Thr	Ile	Arg	Gln	Gln	Ile	Met	Gln	Leu	Lys	Ile	Met
			450			455					460			Thr
Asn	Arg	Leu	Arg	Gly	Ala	Tyr	Gly	Gly	Asn	Asp	Val	Asp	Phe	Gln
465					470				475					480
Ala	Ser	Asp	Asp	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Gly	Gly	Cys	Pro
				485					490					495
Asp	Ala	Cys	Gly	Arg	Arg	Val	Ser	Lys	Lys	Ser	Ser	Ser	Ser	Arg
			500					505					510	Thr
Pro	Leu	Thr	His	Ala	Leu	Pro	Gly	Leu	Ser	Glu	Gln	Glu	Gly	Gln
			515				520					525		Lys

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Thr Ser Ala
530

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGCTGGGAG GTGTCATTGC TGGAGGCCTG GTGGGCCTCA TCTTTGCTGT GTGCCTGGTG 60
GCTTTCATGC TATAC 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCCTAGCAG CTGTCATTGC TGGTGGAGTT ATTGGCTTTC TCTTTGCAAT TTTTCTTATC 60
CTGCTGTTGG TG 72

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Leu Ala Ala Val Ile Ala Gly Gly Val Ile Gly Phe Leu Phe Ala
1 5 10 15
Ile Phe Leu Ile Leu Leu Val
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTGTTGATAG CTGTGATTGT CGGCGGTGTG GTGGGAGCCC TCTTTGCTGC CTTCTTGTC 60
ATGCTGCTCA TCTAC 75

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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GTCTTGGCAG CTCTGATTGT GGGCGGCGTA GTGGGCATCC TCTTCGCCGT TTTCCTGATC 60
CTGCTGCTGG TGTAC 75

(2) INFORMATION FOR SEQ ID NO:13:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCGCCACTC GCCCAGAGCC TCACTACTTC TTTCTGCTCT TCCTGTTTAC CTTGGTCCTT 60
GCTGCAGCCA GGGCCAGGTG GCGGTAACGTG CCC 93

(2) INFORMATION FOR SEQ ID NO:14:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala	Thr	Arg	Pro	Glu	Pro	His	Tyr	Phe	Phe	Leu	Leu	Phe	Leu	Phe	Thr
1				5					10					15	
Leu	Val	Leu	Ala	Ala	Ala	Arg	Pro	Arg	Trp	Arg					
			20						25						

(2) INFORMATION FOR SEQ ID NO:15:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGCGACACT GCTCATCCCA GCCATCACGA CTGCTGACGC CGGCTTCTAC CTCTGCGTGG 60
CCACCAGCCC TGCAGGCACT GCC 83

(2) INFORMATION FOR SEQ ID NO:16:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCATGAAGA AGAAGGATGA AGGCAGTTAC GACTTGGGCA AGAAACCCAT CTACAAAAAA 60
GCCCCACCA ACGAGTTCTA CGCATGA 87

(2) INFORMATION FOR SEQ ID NO:17:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

- 2 -

Leu Gly Lys Lys Pro Ile Tyr Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCCGCCAGC AAGAGCCGGA GCT

23

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTGAGGCTCT GGGCGAGTGG GGG

23

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATAGAGCTCT TGGAAACCATG GCGCCTGTCT GCC

33

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCAG GTTTTATTAT CTTTTTATC

29

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGTATTGGGC GCCGTGTCAC CAGGGC

26

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCCATGAGC TCCACCACCC TGTTCC

26

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Leu Gly Lys Lys Pro Ile Tyr Lys Lys

1

5

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